

SEQUENCE LISTING

<110> Lok, Si
Holloway, James L.

<120> Human V2 Vomeronasal Receptor

<130> 00-107

<150> 60/252,373
<151> 2000-11-21

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 657
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(657)

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Met Phe Glu Arg Arg Lys Glu Gln Asp Glu Gly Pro Gly Ile His Glu
1 5 10 15

ttt ctt gca ttt tta tgg gct gaa ttg ggc tct gaa gcc aaa gaa gag 96
Phe Leu Ala Phe Leu Trp Ala Glu Leu Gly Ser Glu Ala Lys Glu Glu
20 25 30

aaa gaa gaa gaa cgg acc tgc cgg ttg ctg ggc aag tgt gta gat gcc 144
Lys Glu Glu Arg Thr Cys Arg Leu Leu Gly Lys Cys Val Asp Ala
35 40 45

gaa aac cat tcc ctt gtt att gga gga ctg ttt cct att gac tcc agg 192
Glu Asn His Ser Leu Val Ile Gly Gly Leu Phe Pro Ile Asp Ser Arg
50 55 60

acc atc cca gca aat gag tct att ttg gag cca gca tca gca aaa tgt			240
Thr Ile Pro Ala Asn Glu Ser Ile Leu Glu Pro Ala Ser Ala Lys Cys			
65	70	75	80
gaa ggg ttt aac ttt cag aga ttc cgc tgg atg aaa gcc atg atc cac			288
Glu Gly Phe Asn Phe Gln Arg Phe Arg Trp Met Lys Ala Met Ile His			
85	90	95	
atg atc aag gag att aat aag agg aag gat att ttg ccc aac atc act			336
Met Ile Lys Glu Ile Asn Lys Arg Lys Asp Ile Leu Pro Asn Ile Thr			
100	105	110	
ctg ggc tat cag atc ttt gat acc tgt ttt acc atc tcc aaa tca gtg			384
Leu Gly Tyr Gln Ile Phe Asp Thr Cys Phe Thr Ile Ser Lys Ser Val			
115	120	125	
gaa gca gtc ttg gta ttt ctt aca ggg cag gaa gaa aac agg ccc aat			432
Glu Ala Val Leu Val Phe Leu Thr Gly Gln Glu Glu Asn Arg Pro Asn			
130	135	140	
ttt aga aac agc act gga gca ttt ccg gca gga att gtt gga gca ggt			480
Phe Arg Asn Ser Thr Gly Ala Phe Pro Ala Gly Ile Val Gly Ala Gly			
145	150	155	160
gga tca ttc tta tca gtt cct gct tca aga att cta ggg tta tat tat			528
Gly Ser Phe Leu Ser Val Pro Ala Ser Arg Ile Leu Gly Leu Tyr Tyr			
165	170	175	
ttg cct cag gtg ggc tat acc tct acc tgc gtg att ctt agt gac aaa			576
Leu Pro Gln Val Gly Tyr Thr Ser Thr Cys Val Ile Leu Ser Asp Lys			
180	185	190	
tac cag ttt cca tct tat ctt cgt gta ata gcc agc gat aag atc cag			624
Tyr Gln Phe Pro Ser Tyr Leu Arg Val Ile Ala Ser Asp Lys Ile Gln			
195	200	205	
tcg aag gct gtg gta aaa cgt atc caa cac ttt			657
Ser Lys Ala Val Val Lys Arg Ile Gln His Phe			
210	215		
<210> 2			
<211> 219			
<212> PRT			

<213> Homo sapiens

<400> 2

Met	Phe	Glu	Arg	Arg	Lys	Glu	Gln	Asp	Glu	Gly	Pro	Gly	Ile	His	Glu
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														15	
Phe	Leu	Ala	Phe	Leu	Trp	Ala	Glu	Leu	Gly	Ser	Glu	Ala	Lys	Glu	Glu
														30	
Lys	Glu	Glu	Glu	Arg	Thr	Cys	Arg	Leu	Leu	Gly	Lys	Cys	Val	Asp	Ala
														45	
Glu	Asn	His	Ser	Leu	Val	Ile	Gly	Gly	Leu	Phe	Pro	Ile	Asp	Ser	Arg
														55	60
50															
Thr	Ile	Pro	Ala	Asn	Glu	Ser	Ile	Leu	Glu	Pro	Ala	Ser	Ala	Lys	Cys
65														80	
Glu	Gly	Phe	Asn	Phe	Gln	Arg	Phe	Arg	Trp	Met	Lys	Ala	Met	Ile	His
														95	
Met	Ile	Lys	Glu	Ile	Asn	Lys	Arg	Lys	Asp	Ile	Leu	Pro	Asn	Ile	Thr
100														110	
Leu	Gly	Tyr	Gln	Ile	Phe	Asp	Thr	Cys	Phe	Thr	Ile	Ser	Lys	Ser	Val
115														125	
Glu	Ala	Val	Leu	Val	Phe	Leu	Thr	Gly	Gln	Glu	Glu	Asn	Arg	Pro	Asn
130														140	
Phe	Arg	Asn	Ser	Thr	Gly	Ala	Phe	Pro	Ala	Gly	Ile	Val	Gly	Ala	Gly
145														160	
Gly	Ser	Phe	Leu	Ser	Val	Pro	Ala	Ser	Arg	Ile	Leu	Gly	Leu	Tyr	Tyr
165														175	
Leu	Pro	Gln	Val	Gly	Tyr	Thr	Ser	Thr	Cys	Val	Ile	Leu	Ser	Asp	Lys
180														190	
Tyr	Gln	Phe	Pro	Ser	Tyr	Leu	Arg	Val	Ile	Ala	Ser	Asp	Lys	Ile	Gln
195														205	
Ser	Lys	Ala	Val	Val	Lys	Arg	Ile	Gln	His	Phe					
210															
215															

<210> 3

<211> 657

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:2.

<221> misc_feature

<222> 12, 15, 33, 36, 39, 54, 57, 63, 69, 75, 78, 81, 87, 111,

114, 120, 123, 126, 129, 138, 144, 156, 159, 162, 168, 171,
 174, 180, 189, 192, 195, 201, 204, 213, 219, 225, 228, 231,
 234, 246, 261, 267, 279, 312, 324, 327, 336, 339, 342

<223> n = A,T,C or G

<221> misc_feature

<222> 360, 369, 375, 381, 384, 390, 393, 396, 399, 405, 408, 411,
 426, 429, 438, 444, 447, 450, 453, 459, 462, 465, 471, 474,
 477, 480, 483, 486, 492, 495, 498, 501, 504, 507, 510, 516,
 519, 522, 531, 534, 540, 543, 549, 552, 555, 561, 567

<223> n = A,T,C or G

<221> misc_feature

<222> 570, 588, 591, 597, 600, 603, 609, 612, 627, 633, 636, 639,
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<223> n = A,T,C or G

<400> 3

atgtygarm gnmnaarga rcargaygar ggnccngna thcaygartt yytngcnty 60
 ytnntggcng arytnnnws ngargcnaar gargaaraarg argargarmg nacntgymgn 120
 ytnytngna artgygtnga ycngaraay caywsnytng tnathggng nytnnccn 180
 athgaywsnm gnacnathcc ngcnaaygar wsnathtyng arccngcnws ngcnaartgy 240
 garginntya ayttycarmg ntymgntgg atgaargcna tgathcayat gathaargar 300
 athaayaarm gnaargayat hytnccnaay athacnytng gntaycarat httygayach 360
 tgyttaacna thwsnaarws ntngargcn gtnytngtnt tyytnacngg ncargargar 420
 aaymgnccna ayttymgnaa ywsnacnggn gcnttyccng cnggnathgt ngngcnggn 480
 ggnwsnttuy tnwsngtncc ngcwsnmgn athytngny tntaytayyt nccncargtn 540
 ggntayacnw snacntgygt nathytnwsn gayaartayc arttycnwts ntaytnmgn 600
 gtnathgcnw sngayaarat hcarwsnaar gcngtngtta armgnathca rcaytty 657

<210> 4

<211> 1140

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1140)

<400> 4

ctt ccc cat tca gtg tgt act gat gtg tgt cct cct ggg act gga agg 48
 Leu Pro His Ser Val Cys Thr Asp Val Cys Pro Pro Gly Thr Gly Arg

1

5

10

15

gga ttc gtt cag agg gaa cca ata tgc tgc ttt gac tcc atc cca tgt Gly Phe Val Gln Arg Glu Pro Ile Cys Cys Phe Asp Ser Ile Pro Cys 20 25 30	96
gct gat gga cac gtg tca cgg aaa cca ggt gaa agg gag tgt gaa caa Ala Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu Cys Glu Gln 35 40 45	144
tgt ggt gaa gac tat tgg tca aat gca caa aag agc gag tgt gtg ctg Cys Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu Cys Val Leu 50 55 60	192
aaa gag gtg gaa tac ctt gct tat gat gag gcc ctg gga ttc aca ctt Lys Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly Phe Thr Leu 65 70 75 80	240
gtc att ctt tct gtc ttt ggg gca ttt gtg gtc ttg gca gtc aca gct Val Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala Val Thr Ala 85 90 95	288
gtg tat gtg ata cac agg cac act ccc ctg gtg aac gcc agt gac tgg Val Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala Ser Asp Trp 100 105 110	336
cag ctg ggc ttt ctc att cag gtt tct ctg atc atc atg ctg ctg tcg Gln Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met Leu Leu Ser 115 120 125	384
tcc atg ctt ttc att gac aag cca cac aac tgg tcc tgc atg gct ggc Ser Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys Met Ala Gly 130 135 140	432
cag gtc act ctg gca ctg ggc ttt tct ctt tgc ctg tct tgc ctt ctt Gln Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser Cys Leu Leu 145 150 155 160	480
gga aag act agt tca ctg ttt tta gcc tac aga att tcc aaa tcc aaa Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser Lys Ser Lys 165 170 175	528
act caa ctt aca tcc atg cac ccc ctt tat cggttaaaattgtgcta	576

Thr Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile Ile Val Leu			
180	185	190	
atc tct gtt cta gcg gag att ggc ata tgt aca gcc tac ttg ata ttg			624
Ile Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr Leu Ile Leu			
195	200	205	
gaa cct ccc atg gta tac aag aac atg gaa tct caa aat aca aag atc			672
Glu Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn Thr Lys Ile			
210	215	220	
att ctg gga tgc aat gaa att tcc ata gag ttt ttg tac tcg atg ttt			720
Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr Ser Met Phe			
225	230	235	240
gga att gat gcc ttc tta gcc ttg cta tgc ttt ctt aca act ttt gtg			768
Gly Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr Thr Phe Val			
245	250	255	
gct cgc cag tta cca gat aat tac tat gaa gga aaa tgc atc acc ttt			816
Ala Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys Ile Thr Phe			
260	265	270	
ggg atg ctt gtc ttt ttc atc att tgg atg tct ttt gtc cct gtt tat			864
Gly Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val Pro Val Tyr			
275	280	285	
ttg agc acc aaa ggc aag ttc aaa atg gct gtg gaa ata ttt gca atc			912
Leu Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile Phe Ala Ile			
290	295	300	
ttg gca tcc agc cat ggc ttg ttg ggt tgt ata ttt gct cct aag tgc			960
Leu Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala Pro Lys Cys			
305	310	315	320
ctc att att ttg ctg agg cca gag agg aac acc agt gaa att gtt tgt			1008
Leu Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu Ile Val Cys			
325	330	335	
gga aga gtc tcc acc aca gat aat tgc atc caa ctg acc tca gct ttt			1056
Gly Arg Val Ser Thr Thr Asp Asn Cys Ile Gln Leu Thr Ser Ala Phe			
340	345	350	

gtg agc agt gag ctt aac aat acc aca gtg tca act gtt ctg gat gac 1104
 Val Ser Ser Glu Leu Asn Asn Thr Thr Val Ser Thr Val Leu Asp Asp
 355 360 365

aga gtt ttg att tac atg tgt cct ttg aag ctg caa 1140
 Arg Val Leu Ile Tyr Met Cys Pro Leu Lys Leu Gln
 370 375 380

<210> 5
 <211> 380
 <212> PRT
 <213> Homo sapiens

<400> 5
 Leu Pro His Ser Val Cys Thr Asp Val Cys Pro Pro Gly Thr Gly Arg
 1 5 10 15
 Gly Phe Val Gln Arg Glu Pro Ile Cys Cys Phe Asp Ser Ile Pro Cys
 20 25 30
 Ala Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu Cys Glu Gln
 35 40 45
 Cys Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu Cys Val Leu
 50 55 60
 Lys Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly Phe Thr Leu
 65 70 75 80
 Val Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala Val Thr Ala
 85 90 95
 Val Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala Ser Asp Trp
 100 105 110
 Gln Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met Leu Leu Ser
 115 120 125
 Ser Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys Met Ala Gly
 130 135 140
 Gln Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser Cys Leu Leu
 145 150 155 160
 Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser Lys Ser Lys
 165 170 175
 Thr Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile Ile Val Leu
 180 185 190
 Ile Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr Leu Ile Leu
 195 200 205
 Glu Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn Thr Lys Ile
 210 215 220

Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr Ser Met Phe
 225 230 235 240
 Gly Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr Thr Phe Val
 245 250 255
 Ala Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys Ile Thr Phe
 260 265 270
 Gly Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val Pro Val Tyr
 275 280 285
 Leu Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile Phe Ala Ile
 290 295 300
 Leu Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala Pro Lys Cys
 305 310 315 320
 Leu Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu Ile Val Cys
 325 330 335
 Gly Arg Val Ser Thr Thr Asp Asn Cys Ile Gln Leu Thr Ser Ala Phe
 340 345 350
 Val Ser Ser Glu Leu Asn Asn Thr Thr Val Ser Thr Val Leu Asp Asp
 355 360 365
 Arg Val Leu Ile Tyr Met Cys Pro Leu Lys Leu Gln
 370 375 380

<210> 6

<211> 1140

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:5.

<221> misc_feature

<222> 3, 6, 12, 15, 21, 27, 33, 36, 39, 42, 45, 48, 51, 57, 63, 69, 87, 93, 99, 105, 111, 114, 117, 123, 126, 132, 150, 165, 171, 180, 189, 192, 201, 210, 213, 225, 228, 231, 237, 240, 243, 249, 252, 255, 261, 264, 270, 273, 276, 279, 282

<223> n = A,T,C or G

<221> misc_feature

<222> 285, 288, 291, 297, 306, 312, 315, 318, 321, 327, 330, 342, 345, 351, 360, 363, 366, 378, 381, 384, 387, 393, 408, 420, 429, 432, 438, 441, 444, 447, 450, 453, 459, 462, 468, 471, 477, 480, 483, 489, 492, 495, 498, 504, 507, 513, 519

<223> n = A,T,C or G

<221> misc_feature

<222> 525, 531, 537, 540, 543, 552, 555, 561, 573, 576, 582, 585, 588, 591, 600, 609, 612, 618, 624, 630, 633, 639, 657, 666, 678, 681, 696, 708, 714, 723, 732, 738, 741, 744, 747, 756, 759, 762, 768, 771, 774, 780, 783, 801, 813, 819, 825

<223> n = A,T,C or G

<221> misc_feature

<222> 828, 849, 855, 858, 861, 867, 870, 873, 879, 894, 897, 909, 915, 918, 921, 924, 930, 933, 936, 939, 951, 954, 963, 972, 975, 978, 981, 987, 993, 996, 1005, 1011, 1014, 1017, 1020, 1023, 1026, 1044, 1047, 1050, 1053, 1059, 1062, 1065

<223> n = A,T,C or G

<221> misc_feature

<222> 1071, 1080, 1083, 1086, 1089, 1092, 1095, 1098, 1107, 1110, 1113, 1128, 1131, 1137

<223> n = A,T,C or G

<400> 6

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 ccngngarm gngartgyga rcartgyggn gargaytayt ggwsnaaygc ncaraarwsn 180
 gartgygtny tnaargargt ngartayytn gcntaygag argcnytngg nttyacnytn 240
 gtnathytnw sngtnttygg ncntytygtn gtntyngcng tnacngcngt ntaygtnath 300
 caymgnaya cnccnytngt naaygcnwsn gaytggcary tngnttyyt nathcargtn 360
 wsnytnatha thatgytnyt nwsnwsnatg ytnttyathg ayaarcnca yaaytggwsn 420
 tgyatggcng gncargtnac nyngcnytn ggnttywsny tntgyytnws ntgyytnytn 480
 ggnaraacnw snwsnytntt yytngcntay mgnathwsna arwsnaarac ncarytnacn 540
 wsnatgcayc cnytntaymg naarathath gtntytnathw sngtntyngc ngarathggn 600
 athtgyacng cntayytnat hytngarccn ccnatggnt ayaaraayat ggarwsncar 660
 aayacnaara thathytngg ntgyaaygar athwsnathg artyytnta ywsnatgtyt 720
 ggnathgag yntyytngc nyntyntgy tyytncna cntyytngc nmgnacrytn 780
 ccngayaayt aytaygargg naartgyath acntyygna tgytngtntt yttyathath 840
 tggatgwsnt tygtntcngt ntayytnwsn acnaarggna artyaarat ggcngtngar 900
 athtgycna thytngcnws nwncayggn ytnytnngnt gyathtgygc nccnaartgy 960
 ytnathathy tnytnmgncc ngarmgnaay acnwsngara thgtntgygg nmgngrtnwsn 1020
 acnacngaya aytgyathca rytnacnwsn gcntyytngt snwsngaryt naayaayacn 1080
 acngtnwsna cngtntyngt ygaymgnngt ytnathtaya tgtgycnyt naarytnca 1140

<210> 7

<211> 2781

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric receptor.

<221> CDS

<222> (1)...(2781)

<400> 7

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Met	Phe	Glu	Arg	Arg	Lys	Glu	Gln	Asp	Glu	Gly	Pro	Gly	Ile	His	Glu	
1	5												10	15		

ttt	ctt	gca	ttt	tta	tgg	gct	gaa	ttg	ggc	tct	gaa	gcc	aaa	gaa	gag	96
Phe	Leu	Ala	Phe	Leu	Trp	Ala	Glu	Leu	Gly	Ser	Glu	Ala	Lys	Glu	Glu	
20	25												30			

aaa	gaa	gaa	cg	acc	tgc	cg	ttg	ctg	ggc	aag	tgt	gta	gat	gcc	144	
Lys	Glu	Glu	Glu	Arg	Thr	Cys	Arg	Leu	Leu	Gly	Lys	Cys	Val	Asp	Ala	
35													45			

gaa	aac	cat	tcc	ctt	gtt	att	gga	gga	ctg	ttt	cct	att	gac	tcc	agg	192
Glu	Asn	His	Ser	Leu	Val	Ile	Gly	Gly	Leu	Phe	Pro	Ile	Asp	Ser	Arg	
50													60			

acc	atc	cca	gca	aat	gag	tct	att	ttg	gag	cca	gca	tca	gca	aaa	tgt	240
Thr	Ile	Pro	Ala	Asn	Glu	Ser	Ile	Leu	Glu	Pro	Ala	Ser	Ala	Lys	Cys	
65													75	80		

gaa	ggg	ttt	aac	ttt	cag	aga	ttc	cg	tgg	atg	aaa	gcc	atg	atc	cac	288
Glu	Gly	Phe	Asn	Phe	Gln	Arg	Phe	Arg	Trp	Met	Lys	Ala	Met	Ile	His	
85													95			

atg	atc	aag	gag	att	aat	aag	agg	aag	gat	att	ttg	ccc	aac	atc	act	336
Met	Ile	Lys	Glu	Ile	Asn	Lys	Arg	Lys	Asp	Ile	Leu	Pro	Asn	Ile	Thr	
100													105	110		

ctg	ggc	tat	cag	atc	ttt	gat	acc	tgt	ttt	acc	atc	tcc	aaa	tca	gtg	384
Leu	Gly	Tyr	Gln	Ile	Phe	Asp	Thr	Cys	Phe	Thr	Ile	Ser	Lys	Ser	Val	
115													125			

gaa	gca	gtc	ttg	gta	ttt	ctt	aca	ggg	cag	gaa	gaa	aac	agg	ccc	aat	432
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Glu Ala Val Leu Val Phe Leu Thr Gly Gln Glu Glu Asn Arg Pro Asn			
130	135	140	
ttt aga aac agc act gga gca ttt ccg gca gga att gtt gga gca ggt			480
Phe Arg Asn Ser Thr Gly Ala Phe Pro Ala Gly Ile Val Gly Ala Gly			
145	150	155	160
gga tca ttc tta tca gtt cct gct tca aga att cta ggg tta tat tat			528
Gly Ser Phe Leu Ser Val Pro Ala Ser Arg Ile Leu Gly Leu Tyr Tyr			
165	170	175	
ttg cct cag gtg ggc tat acc tct acc tgc gtg att ctt agt gac aaa			576
Leu Pro Gln Val Gly Tyr Thr Ser Thr Cys Val Ile Leu Ser Asp Lys			
180	185	190	
tac cag ttt cca tct tat ctt cgt gta ata gcc agc gat aag atc cag			624
Tyr Gln Phe Pro Ser Tyr Leu Arg Val Ile Ala Ser Asp Lys Ile Gln			
195	200	205	
tcg aag gct gtg gta aaa cgt atc caa cac ttt ggt tgg gtc tgg gta			672
Ser Lys Ala Val Val Lys Arg Ile Gln His Phe Gly Trp Val Trp Val			
210	215	220	
ggt gct att gca gct gat gat tat ggg aaa tat gga gta aaa act			720
Gly Ala Ile Ala Ala Asp Asp Asp Tyr Gly Lys Tyr Gly Val Lys Thr			
225	230	235	240
ttt aag gaa aaa atg gag agt gcc aac ctc tgt gtt gct ttc tct gaa			768
Phe Lys Glu Lys Met Glu Ser Ala Asn Leu Cys Val Ala Phe Ser Glu			
245	250	255	
acc att ccc aaa gtc tac tcc aat gag aaa atg cag aag gct gtt aag			816
Thr Ile Pro Lys Val Tyr Ser Asn Glu Lys Met Gln Lys Ala Val Lys			
260	265	270	
gca gta aag act tcc act gcc aaa gtc att gtg ctt tat act tct gac			864
Ala Val Lys Thr Ser Thr Ala Lys Val Ile Val Leu Tyr Thr Ser Asp			
275	280	285	
att gac ctc agc ctg ttt gtg ctg gaa atg att cat cat aac ata act			912
Ile Asp Leu Ser Leu Phe Val Leu Glu Met Ile His His Asn Ile Thr			
290	295	300	

gac agg aca tgg ata gcc acc gaa gcc tgg att acc tct gct ctc att Asp Arg Thr Trp Ile Ala Thr Glu Ala Trp Ile Thr Ser Ala Leu Ile 305	310	315	320	960
gca aag cct gag tat ttc ccc tat ttt ggt gga act att gga ttt gca Ala Lys Pro Glu Tyr Phe Pro Tyr Phe Gly Gly Thr Ile Gly Phe Ala 325	330	335		1008
aca cca aga agt gtt ata cca gga cta aaa gaa ttt ctt tat gat gta Thr Pro Arg Ser Val Ile Pro Gly Leu Lys Glu Phe Leu Tyr Asp Val 340	345	350		1056
cac cct aac aag gat cca aat gat gtc ttg acc att gaa ttc tgg caa His Pro Asn Lys Asp Pro Asn Asp Val Leu Thr Ile Glu Phe Trp Gln 355	360	365		1104
act gct ttt aac tgt acc tgg ccc aac agc agt gtt cct tat aac gtg Thr Ala Phe Asn Cys Thr Trp Pro Asn Ser Ser Val Pro Tyr Asn Val 370	375	380		1152
gat cac aga gtg aat atg act ggg aaa gaa gac aga ctg tat gac atg Asp His Arg Val Asn Met Thr Gly Lys Glu Asp Arg Leu Tyr Asp Met 385	390	395	400	1200
tct gat cag ctc tgc act gga gag gag aag ctg gaa gat ctg aaa aac Ser Asp Gln Leu Cys Thr Gly Glu Lys Leu Glu Asp Leu Lys Asn 405	410		415	1248
acc tat ctg gat aca tca cag cta aga att aca aaa caa tgt aaa caa Thr Tyr Leu Asp Thr Ser Gln Leu Arg Ile Thr Lys Gln Cys Lys Gln 420	425	430		1296
gct gta tat gct ata gct cat ggc ctg gat cat ctc agc aga tgt caa Ala Val Tyr Ala Ile Ala His Gly Leu Asp His Leu Ser Arg Cys Gln 435	440	445		1344
gaa ggg cag gga cca ttt ggc tca aat cag caa tgt gca tat ata cct Glu Gly Gln Gly Pro Phe Gly Ser Asn Gln Gln Cys Ala Tyr Ile Pro 450	455	460		1392
acc ttt gat ttc tgg cag cta atg tac tat atg aaa gaa att aaa ttt Thr Phe Asp Phe Trp Gln Leu Met Tyr Tyr Met Lys Glu Ile Lys Phe 465	470	475	480	1440

aaa tca cat gag gat aaa tgg gta att ctg gat gat aat gga gat ttg Lys Ser His Glu Asp Lys Trp Val Ile Leu Asp Asp Asn Gly Asp Leu 485 490 495	1488
aaa aat gga cac tat gat gtc cta aac tgg cac tta gat gat gag gga Lys Asn Gly His Tyr Asp Val Leu Asn Trp His Leu Asp Asp Glu Gly 500 505 510	1536
gaa att tcc ttt gtg aca gtt ggg aga ttt aac ttt aga tct aca aac Glu Ile Ser Phe Val Thr Val Gly Arg Phe Asn Phe Arg Ser Thr Asn 515 520 525	1584
ttt gag ctt gtt att cca acg aat tct aca ata ttt tgg aac act gag Phe Glu Leu Val Ile Pro Thr Asn Ser Thr Ile Phe Trp Asn Thr Glu 530 535 540	1632
tca tca agg ctt ccc cat tca gtg tgt act gat gtg tgt cct cct ggg Ser Ser Arg Leu Pro His Ser Val Cys Thr Asp Val Cys Pro Pro Gly 545 550 555 560	1680
act gga agg gga ttc gtt cag agg gaa cca ata tgc tgc ttt gac tcc Thr Gly Arg Gly Phe Val Gln Arg Glu Pro Ile Cys Cys Phe Asp Ser 565 570 575	1728
atc cca tgt gct gat gga cac gtg tca cgg aaa cca ggt gaa agg gag Ile Pro Cys Ala Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu 580 585 590	1776
tgt gaa caa tgt ggt gaa gac tat tgg tca aat gca caa aag agc gag Cys Glu Gln Cys Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu 595 600 605	1824
tgt gtg ctg aaa gag gtg gaa tac ctt gct tat gat gag gcc ctg gga Cys Val Leu Lys Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly 610 615 620	1872
ttc aca ctt gtc att ctt tct gtc ttt ggg gca ttt gtg gtc ttg gca Phe Thr Leu Val Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala 625 630 635 640	1920
gtc aca gct gtg tat gtg ata cac agg cac act ccc ctg gtg aac gcc	1968

Val Thr Ala Val Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala			
645	650	655	
agt gac tgg cag ctg ggc ttt ctc att cag gtt tct ctg atc atc atg			2016
Ser Asp Trp Gln Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met			
660	665	670	
ctg ctg tcg tcc atg ctt ttc att gac aag cca cac aac tgg tcc tgc			2064
Leu Leu Ser Ser Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys			
675	680	685	
atg gct ggc cag gtc act ctg gca ctg ggc ttt tct ctt tgc ctg tct			2112
Met Ala Gly Gln Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser			
690	695	700	
tgc ctt ctt gga aag act agt tca ctg ttt tta gcc tac aga att tcc			2160
Cys Leu Leu Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser			
705	710	715	720
aaa tcc aaa act caa ctt aca tcc atg cac ccc ctt tat cgg aaa atc			2208
Lys Ser Lys Thr Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile			
725	730	735	
att gtg cta atc tct gtt cta gcg gag att ggc ata tgt aca gcc tac			2256
Ile Val Leu Ile Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr			
740	745	750	
ttg ata ttg gaa cct ccc atg gta tac aag aac atg gaa tctcaa aat			2304
Leu Ile Leu Glu Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn			
755	760	765	
aca aag atc att ctg gga tgc aat gaa att tcc ata gag ttt ttg tac			2352
Thr Lys Ile Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr			
770	775	780	
tcg atg ttt gga att gat gcc ttc tta gcc ttg cta tgc ttt ctt aca			2400
Ser Met Phe Gly Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr			
785	790	795	800
act ttt gtg gct cgc cag tta cca gat aat tac tat gaa gga aaa tgc			2448
Thr Phe Val Ala Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys			
805	810	815	

atc acc ttt ggg atg ctt gtc ttt ttc atc att tgg atg tct ttt gtc Ile Thr Phe Gly Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val	820	825	830	2496
cct gtt tat ttg agc acc aaa ggc aag ttc aaa atg gct gtg gaa ata Pro Val Tyr Leu Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile	835	840	845	2544
ttt gca atc ttg gca tcc agc cat ggc ttg ttg ggt tgt ata ttt gct Phe Ala Ile Leu Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala	850	855	860	2592
cct aag tgc ctc att att ttg ctg agg cca gag agg aac acc agt gaa Pro Lys Cys Leu Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu	865	870	875	2640
att gtt tgt gga aga gtc tcc acc aca gat aat tgc atc caa ctg acc Ile Val Cys Gly Arg Val Ser Thr Thr Asp Asn Cys Ile Gln Leu Thr	885	890	895	2688
tca gct ttt gtg agc agt gag ctt aac aat acc aca gtg tca act gtt Ser Ala Phe Val Ser Ser Glu Leu Asn Asn Thr Thr Val Ser Thr Val	900	905	910	2736
ctg gat gac aga gtt ttg att tac atg tgt cct ttg aag ctg caa Leu Asp Asp Arg Val Leu Ile Tyr Met Cys Pro Leu Lys Leu Gln	915	920	925	2781
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<213> Artificial Sequence				
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<223> Chimeric receptor.				
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Met Phe Glu Arg Arg Lys Glu Gln Asp Glu Gly Pro Gly Ile His Glu	1	5	10	15
Phe Leu Ala Phe Leu Trp Ala Glu Leu Gly Ser Glu Ala Lys Glu Glu	20	25	30	

Lys Glu Glu Glu Arg Thr Cys Arg Leu Leu Gly Lys Cys Val Asp Ala
 35 40 45
 Glu Asn His Ser Leu Val Ile Gly Gly Leu Phe Pro Ile Asp Ser Arg
 50 55 60
 Thr Ile Pro Ala Asn Glu Ser Ile Leu Glu Pro Ala Ser Ala Lys Cys
 65 70 75 80
 Glu Gly Phe Asn Phe Gln Arg Phe Arg Trp Met Lys Ala Met Ile His
 85 90 95
 Met Ile Lys Glu Ile Asn Lys Arg Lys Asp Ile Leu Pro Asn Ile Thr
 100 105 110
 Leu Gly Tyr Gln Ile Phe Asp Thr Cys Phe Thr Ile Ser Lys Ser Val
 115 120 125
 Glu Ala Val Leu Val Phe Leu Thr Gly Gln Glu Glu Asn Arg Pro Asn
 130 135 140
 Phe Arg Asn Ser Thr Gly Ala Phe Pro Ala Gly Ile Val Gly Ala Gly
 145 150 155 160
 Gly Ser Phe Leu Ser Val Pro Ala Ser Arg Ile Leu Gly Leu Tyr Tyr
 165 170 175
 Leu Pro Gln Val Gly Tyr Thr Ser Thr Cys Val Ile Leu Ser Asp Lys
 180 185 190
 Tyr Gln Phe Pro Ser Tyr Leu Arg Val Ile Ala Ser Asp Lys Ile Gln
 195 200 205
 Ser Lys Ala Val Val Lys Arg Ile Gln His Phe Gly Trp Val Trp Val
 210 215 220
 Gly Ala Ile Ala Ala Asp Asp Asp Tyr Gly Lys Tyr Gly Val Lys Thr
 225 230 235 240
 Phe Lys Glu Lys Met Glu Ser Ala Asn Leu Cys Val Ala Phe Ser Glu
 245 250 255
 Thr Ile Pro Lys Val Tyr Ser Asn Glu Lys Met Gln Lys Ala Val Lys
 260 265 270
 Ala Val Lys Thr Ser Thr Ala Lys Val Ile Val Leu Tyr Thr Ser Asp
 275 280 285
 Ile Asp Leu Ser Leu Phe Val Leu Glu Met Ile His His Asn Ile Thr
 290 295 300
 Asp Arg Thr Trp Ile Ala Thr Glu Ala Trp Ile Thr Ser Ala Leu Ile
 305 310 315 320
 Ala Lys Pro Glu Tyr Phe Pro Tyr Phe Gly Gly Thr Ile Gly Phe Ala
 325 330 335
 Thr Pro Arg Ser Val Ile Pro Gly Leu Lys Glu Phe Leu Tyr Asp Val
 340 345 350
 His Pro Asn Lys Asp Pro Asn Asp Val Leu Thr Ile Glu Phe Trp Gln
 355 360 365

Thr Ala Phe Asn Cys Thr Trp Pro Asn Ser Ser Val Pro Tyr Asn Val
 370 375 380
 Asp His Arg Val Asn Met Thr Gly Lys Glu Asp Arg Leu Tyr Asp Met
 385 390 395 400
 Ser Asp Gln Leu Cys Thr Gly Glu Glu Lys Leu Glu Asp Leu Lys Asn
 405 410 415
 Thr Tyr Leu Asp Thr Ser Gln Leu Arg Ile Thr Lys Gln Cys Lys Gln
 420 425 430
 Ala Val Tyr Ala Ile Ala His Gly Leu Asp His Leu Ser Arg Cys Gln
 435 440 445
 Glu Gly Gln Gly Pro Phe Gly Ser Asn Gln Gln Cys Ala Tyr Ile Pro
 450 455 460
 Thr Phe Asp Phe Trp Gln Leu Met Tyr Tyr Met Lys Glu Ile Lys Phe
 465 470 475 480
 Lys Ser His Glu Asp Lys Trp Val Ile Leu Asp Asp Asn Gly Asp Leu
 485 490 495
 Lys Asn Gly His Tyr Asp Val Leu Asn Trp His Leu Asp Asp Glu Gly
 500 505 510
 Glu Ile Ser Phe Val Thr Val Gly Arg Phe Asn Phe Arg Ser Thr Asn
 515 520 525
 Phe Glu Leu Val Ile Pro Thr Asn Ser Thr Ile Phe Trp Asn Thr Glu
 530 535 540
 Ser Ser Arg Leu Pro His Ser Val Cys Thr Asp Val Cys Pro Pro Gly
 545 550 555 560
 Thr Gly Arg Gly Phe Val Gln Arg Glu Pro Ile Cys Cys Phe Asp Ser
 565 570 575
 Ile Pro Cys Ala Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu
 580 585 590
 Cys Glu Gln Cys Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu
 595 600 605
 Cys Val Leu Lys Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly
 610 615 620
 Phe Thr Leu Val Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala
 625 630 635 640
 Val Thr Ala Val Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala
 645 650 655
 Ser Asp Trp Gln Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met
 660 665 670
 Leu Leu Ser Ser Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys
 675 680 685
 Met Ala Gly Gln Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser
 690 695 700

Cys Leu Leu Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser
 705 710 715 720
 Lys Ser Lys Thr Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile
 725 730 735
 Ile Val Leu Ile Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr
 740 745 750
 Leu Ile Leu Glu Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn
 755 760 765
 Thr Lys Ile Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr
 770 775 780
 Ser Met Phe Gly Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr
 785 790 795 800
 Thr Phe Val Ala Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys
 805 810 815
 Ile Thr Phe Gly Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val
 820 825 830
 Pro Val Tyr Leu Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile
 835 840 845
 Phe Ala Ile Leu Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala
 850 855 860
 Pro Lys Cys Leu Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu
 865 870 875 880
 Ile Val Cys Gly Arg Val Ser Thr Thr Asp Asn Cys Ile Gln Leu Thr
 885 890 895
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<213> Artificial Sequence

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<221> misc_feature

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 ytnytnngna artgygtnga ycngaraay caywsnytng tnathggng nytnntyccn 180
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 athaayaarm gnaargayat hytnccnaay athacnytng gntaycarat httygayacn 360
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 aaymgnccna ayttymgnaa ywsnacnggn gcnttyccng cngnathgt ngngcnggn 480
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 gtntaywsna aygaraarat gcaraargcn gtnaargcng tnaaracnws nacngcnaar 840
 gtnathgtny tntayacnws ngayathgay ytnwsnytnt tygtnytna ratgathcay 900
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 wsngtntng cngarathgg nathtgyacn gcntayytna thytngarcc nccnatggtn 2280
 tayaaraaya tggarsnca raayacnaar athathytng gntgyaayga rathwsnath 2340
 garttyytnt aywsnatgtt yggnathgay gnttuytng cnytntng yttiytnacn 2400
 acnttygtng cnmgncaryt nccngayaay taytaygarg gnaartgyat hacnttyggn 2460
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